

Fig. 1

HTRAM.DNA	1	ATGGCGATTG	10	GCAGAGAAAG	20	CACCAAGAGG	30	CCCCCAGTGC	40	TCAGCCACGA	50
KIAA0057.DNA	1	ATGGCTTTCC		GCACGAGGA-		--CGAAAGT		TACCCGCTCT		TCAGCCACGA	50
HWAR1.DNA	1	ATGGGGCTCC		GTAAGAAGAG		CACCAAGAGC		CCCCCGCTTC		TCAGCCACGA	50
RWAR1.DNA	1	ATGGGGCTCC		GCAAGAAGAA		CCCAAGGAGC		CCCCCGGTGC		TCAGCCACGA	50
			60		70		80		90		100
HTRAM.DNA	51	ATTGTCCTCG		CAGAAACACG		CGGACATCGT		CTCCTGTGTG		GGCATGTTCT	100
KIAA0057.DNA	51	GTTCGTGATC		CACAAACATG		CGGACATCGG		CTTCTGCCCTG		GTGCTCTGGG	100
HWAR1.DNA	51	ATTGATCCCTG		CAGAAACATG		CGGACATCGT		CTCCTGCGGTG		GGCATGTTCT	100
RWAR1.DNA	51	ATTGATGGTG		CAGAAACACG		CGGATATGGT		CTCCTGCGGTG		GGCATGTTCT	100
			110		120		130		140		150
HTRAM.DNA	101	TCCTGCTGGG		GCTCATGTTT		GAGATACGGG		CAAAAGCTTC		TATCATTTT	150
KIAA0057.DNA	101	TCCTCATTCG		GCTTATGTTT		GAGGTACAGC		CAAAAGCTTC		CTTCTTATTT	150
HWAR1.DNA	101	TCCTGCTGGG		GCTTGTGTTG		GAGGCAACAG		CAGAAGCATC		CATCGTGTTC	150
RWAR1.DNA	101	TCGTGCTGGG		ACTTATGTTT		GAGGCAACGG		CCAAGATGTC		GATCGTGTTC	150
			160		170		180		190		200
HTRAM.DNA	151	GTACTCTCTC		AGTACATGTT		CACCTCCGCA		GCAACAGAGG		AACAAGCTAC	200
KIAA0057.DNA	151	ATTTTACCTC		AGTATACAT		TAGCTGCCCT		ACAGCAGA--		-----CAG	200
HWAR1.DNA	151	CTCACTCTCTC		AGCAACGTTT		TCTTGTCCTT		GCAGCAGAGG		AACAAGCCAC	200
RWAR1.DNA	151	CTCACCTCTC		AGCATGGAGT		CGTTGTCCC-		--AGCGAAG		GGCTACCTTC	200
			210		220		230		240		250
HTRAM.DNA	201	TGAATCAGTG		TCCCTTTTAT		ACTATGGGAT		CAAAAGATTG		GCTACTGTTT	250
KIAA0057.DNA	201	TGAGAGCGTG		---CACTACC		ACTATGGGCC		TAAAGACCTG		GTCAACATCT	250
HWAR1.DNA	201	GGGTCGAAG		TCCCTCTTAT		ATTATGGTGT		CAAAAGATTG		GCCACGGTTT	250
RWAR1.DNA	201	GGGTCACAG		ACCTTTTACC		ATTATGGGGT		CAAAAGATTG		GCCACAGTGT	250
			260		270		280		290		300
HTRAM.DNA	251	TCTTCTACAT		GCTAGTGGGG		ATAATATTTC		ATGCCGTAAT		TCAAGAGTAT	300
KIAA0057.DNA	251	TGTTCTACAT		CTTCATCACC		ATCATCTTGC		ATGGTGTGGT		TCAGGAGTAC	300
HWAR1.DNA	251	TCTTCTACAT		GCTGGTGGCA		ATCATTTATC		ATGCCACAAI		TCAGGAATAT	300
RWAR1.DNA	251	TCTTCTACAT		GCTGGTGGCC		ATCATCATTC		ACGGCAACAT		TCAGGAGTAC	300
			310		320		330		340		350

Fig. 1 (cont.)

HTRAM. DNA	301	ATGTTGGATA	AAATTAACAG	GCGAATGCAC	TCTCCAAAA	CAAAACACAG	350
KIAA0057. DNA	301	ATTTTAGATA	AAATCAGCAA	ACGGCTTCAT	CTCTCCAAAG	TCAAAACACAG	350
HWAR1. DNA	301	GTGTTGGATA	AAATTAACAA	GAGAATGCAG	TTCAACCAAG	CGAAACAAATA	350
RWAR1. DNA	301	GTGCTAGATA	AGCTCAGCCG	GAGACTGCAG	CTCAACCAAG	GCAAAACAAATA	350
		360	370	380	390	400	
HTRAM. DNA	351	CAAGTTTAAT	GAA TCTGGTC	AGCTTAGTGC	GTTCCTACCTT	TTTTGCTGTG	400
KIAA0057. DNA	351	CAAGTTCAAT	GAATCTGGAC	AGCTGGTCGT	CTTTCATTTTC	ACCTGGTGA	400
HWAR1. DNA	351	CAAGTTTAAC	GAGTCTGGTC	AGTTTAGTGT	GTTCCTACCTT	TTTTCTTGTA	400
RWAR1. DNA	351	CAAAATTGAAT	GAGGCCGGGC	AGCTCAGTGT	GTTCCTACATA	GTCTCTGCTA	400
		410	420	430	440	450	
HTRAM. DNA	401	TTTGGGGCAC	ATTCAATCTTC	ATCTCTGAAA	ACTACATCTTC	AGACCCCAACT	450
KIAA0057. DNA	401	TTTGGTGCCT	CTACCTGGTG	GTGACCGAAG	GATACCTTAAC	AAACCCCAAGA	450
HWAR1. DNA	401	TTTGGGGCAC	ATTCATTTTA	ATCTCTGAAA	ACTGCCCTGTC	AGACCCCAACT	450
RWAR1. DNA	401	TC TGGGGTAT	GATCAATCTG	GCCTCTGAGA	ACTGCCCTGTC	AGACCCCAACT	450
		460	470	480	490	500	
HTRAM. DNA	451	ATCTTATGGA	GGGCTTATCC	CCATAACCTG	ATGACATTTTC	AAATGAAGTT	500
KIAA0057. DNA	451	AGCCTCTGGG	AAGACTACCC	GCATGTGCAC	CTCCCTCTCC	AGGTGAAGTT	500
HWAR1. DNA	451	CTTATATGGA	AGGCTCGTCC	CCATAGCATG	ATGACATTTTC	AAATGAAGTT	500
RWAR1. DNA	451	CTTATTTGGA	AGTCTCAGCC	CCACAACATG	ATGACATTTTC	AGATGAAGTT	500
		510	520	530	540	550	
HTRAM. DNA	501	TTTCTACATA	TCA CAGCTGG	CTTACTGGGT	TCATGCTTTT	CCTGAACTCT	550
KIAA0057. DNA	501	TTTCTACATA	TGC CAGCTGG	CTTACTGGGT	GCACGCACCT	CCTGAACTCT	550
HWAR1. DNA	501	TTTCTACATA	TCC CAGCTGG	CTTACTGGGT	TCATGCTTTT	CCTGAACTCT	550
RWAR1. DNA	501	TTTCTACATC	TCA CAGCTGG	CTTACTGGGT	TCATGCTTTT	CCCGAACTCT	550
		560	570	580	590	600	



09/807470

3/15

Fig. 1 (cont.)

HTRAM.DNA	551	ACTTCCAGAA	AACCAAAA	GAAGAVATTC	CTCGTCAGCT	TGCTACACAT	600
KIAA0057.DNA	551	ACTTCCAGAA	GGTACGGAAG	GAGGAAATTC	CCCGCCAGCT	CCAGTATATTT	600
HWAR1.DNA	551	ACTTCCAGAA	AACCAAAA	CAAGCATCC	CTCGTCAGCT	TGCTACACAT	600
RWAR1.DNA	551	ACTTCCAGAA	AGTCAGGAAA	CAAGAVATTC	CCGCTCAACT	CATCTACACAT	600
HTRAM.DNA	601	GGTCTTTACC	TCTTCCACAT	TGCTGGAGCT	TACCTTTTGA	ACTTGAATCA	650
KIAA0057.DNA	601	TGCCTGTACC	TGGTGCATAT	AGCTGGAGCA	TACCTCTTAA	ACCTGAGCCG	650
HWAR1.DNA	601	GGTCTTACC	TCTTCCACAT	TACTGGAGCT	TATCTCTTGT	ACTTGAATCA	650
RWAR1.DNA	601	GGCTCCACC	TCTTCCACAT	TGAGGGGGCC	TATCTCTTGT	ACTTGAACCA	650
HTRAM.DNA	651	TCTAGGACTT	GTCTTCTGG	TGCTACATTA	TTTGTGTGA	TTTCTTTTCC	700
KIAA0057.DNA	651	CCTGGGCCCTG	ATCTTCTCTG	TGCTGCAGTA	CTCAACTGAG	TTCTCTTTCC	700
HWAR1.DNA	651	TTTGGGACTT	CTTCTTTTGG	TACTGCATTA	TTTGTGTGA	TTTCTTTTCC	700
RWAR1.DNA	651	CCTGGGCCCTG	CTGCTTCTGA	TGCTGCAGTA	TGCTGTCTGAG	CTCTCTTCTCA	700
HTRAM.DNA	701	ACATTTCCCG	CCTGTTTTAT	TTTAGCAATG	AAAAAGTATCA	GAAAGGATTT	750
KIAA0057.DNA	701	ACACGGCTAG	ACTCTTCTAC	TTTGCAGATG	AAAAACAACGA	GAAACTGTTC	750
HWAR1.DNA	701	ACATGTCCCG	CCTGTTTTAC	TTTAGTGAATG	AAAAAGTACCA	GAAAGGCATA	750
RWAR1.DNA	701	GGGTGTGCAG	CCTGCTTTAC	TTTGGGATG	AGCGTACCA	GAAAGGGTTG	750
HTRAM.DNA	751	TCTCTGTGGG	CAGTTCTTTT	TGTTTTGGGA	AGACTTCTGA	CTTTAATTTCT	800
KIAA0057.DNA	751	AGTGCCTGGG	CTGCTGTTTT	TGGGTATACC	CCCTCTTCA	TCCCTCACCCT	800
HWAR1.DNA	751	TCTCTGTGGG	CCATTGTGTT	TATCTTGGGT	AGACTTGTGA	CTTTAATTTCT	800
RWAR1.DNA	751	TCTTTGTGGC	CTATCTGTGTT	TATATCCGGG	AGACTCTGTA	CACTGATTTCT	800
HTRAM.DNA	801	TTTCACTACTG	ACTGTTGGTT	TTGGGCTTGC	AAGACGAGAA	AATCAGAAAC	850
KIAA0057.DNA	801	TGCCGTGCTG	GCCATTGGCT	TTGGACTGGC	TCCCTTGGAA	AACCAAGGCAT	850
HWAR1.DNA	801	TTCCGTACTC	ACTGTTGGGT	TTCACTCTGGC	TGGATGGCAG	AATCGGAATC	850
RWAR1.DNA	801	CTCAGTGGTT	ACAGTAGGGC	TTCACTTGGC	CGGAGCA---	AATCGGAATG	850



Fig. 1 (cont.)

HTRAM.DNA	851	TGGATTTCAG	TACTGGAAC	TCAATGTGT	TAGCTGTTAG	AATCGCTGTT	900
KIAA0057.DNA	851	TTGATCCCGA	GAAGGGAAC	TTCAACACTTT	TGTTTTCAG	GCTCTGCGTG	900
HWAR1.DNA	851	CTGATGCCCT	TACTGGAAT	GTAATGTGT	TGGCAGCTAA	AAATGCTGTT	900
RWAR1.DNA	851	GAATGCTCT	CTCTGTTAT	GTCATGTGT	TGGCAGCTAA	AAATGCTGTT	900
		910	920	930	940	950	
HTRAM.DNA	901	CTGGCATCCA	TTTGGCTTAC	TCAGGCAATT	ATCATGTGGA	AGTTCATTAA	950
KIAA0057.DNA	901	CTCTCTCTGG	TTGTCTCCG	CCAGGCTTGG	CTCATGTGGC	GCTTCATCCA	950
HWAR1.DNA	901	CTGTGCTCCA	CTTGCACCAT	CCAPCCCTAC	GTAACATGGA	ACTTAATTAC	950
RWAR1.DNA	901	CTGTCTCTCCA	CTTGCAGTAT	CCAGTCTTAC	ATAACATGGA	CCTTGACGAC	950
		960	970	980	990	1000	
HTRAM.DNA	951	TTTTCAGCTT	CGAAGGTGGA	GGGAACATTC	TGCTTTTCAG	-GCACAGCTT	1000
KIAA0057.DNA	951	CTCCAGCTTG	CGGCACCTGC	GGGAATCTTG	GAATGAGCAG	AGTGCAAGGC	1000
HWAR1.DNA	951	TCTCTGCTT	CAGAGGTGG	TAGAAGATTC	TAATATTCAG	-GCCATCATGT	1000
RWAR1.DNA	951	CGTCTGCTT	CAGAGATGCT	TAGAAGATTC	GAATCTTCAT	-GTCCT---GT	1000
		1010	1020	1030	1040	1050	
HTRAM.DNA	1001	GTGAAGAAGA	AACCA-ACAG	TACATA-AG	GCAGATCTTC	TAAAAAAGGA	1050
KIAA0057.DNA	1001	GGAGAGTCCC	AGCCACACCC	AGCTATCCAG	CCAGGCTCAT	CAAGAGGGA	1050
HWAR1.DNA	1001	ATGAAAGA	AAC-----GG	TCG-----	--AGATCTTC	TAAAAAAGA	1050
RWAR1.DNA	1001	GGAGGAAGA	GAC-----GG	TC-----	-CAGGTC---	GAGAAAAGGC	1050
		1060	1070	1080	1090	1100	
HTRAM.DNA	1051	ACAGAAATG	GTGTGAATGG	BACATTAAC	TCAAATGTAG	CAGACTCTCC	1100
KIAA0057.DNA	1051	TCTGTTACC	ATGAATAATGG	AGTGGTGAAG	CCAGAGACAG	GAACCTCCCC	1100
HWAR1.DNA	1051	ACAGAAACG	GAGTG---GG	AGTGGAACT	TCAAATAGAG	TAGACTGTCC	1100
RWAR1.DNA	1051	ACAGAAATG	GAGTGCA--G	AA-----T	CCAAATAGAA	TAGATCTCTCC	1100
		1110	1120	1130	1140	1150	
HTRAM.DNA	1101	CCGGAATAAA	AAAGAGAAAT	CTTCA.....	1150
KIAA0057.DNA	1101	ACGCACTAAG	AAACTCAAGT	CTCCC.....	1150
HWAR1.DNA	1101	CCCAAGAGG	AAAGAGAAAT	CTTCA.....	1150
RWAR1.DNA	1101	ACCAAGCAAG	AAAGAGAAAG	CTCCT.....	1150



09/807470

5/15

Fig. 2

HTRAM.AMI	1	MAIRKKSTKS	10	PPVLSHEEVL	20	QNHADIVSCV	30	AMVLLGLME	40	EITAKASTIE	50
KIAA0057.AMI	1	MAFRRR-TKS		YPLFSQEEVI		HNHADIGFQL		VLCVLLGLME		EVTAKTAFLE	50
HWAR1.AMI	1	MGLRKKSTKN		PPVLSQEEIL		QNHADIVSCV		GMFEELGLVE		EGTAESIVE	50
RWAR1.AMI	1	MGLRKKNARN		PPVLSHEEVM		QNHADMVSCV		GMFEVLLGLME		EGTAEMSIVE	50
			60		70		80		90		100
HTRAM.AMI	51	VTLQYNTILE		ATEEQATESV		SLYYGICKDL		ATVFEFVMLVA		IIIIHAVIQEY	100
KIAA0057.AMI	51	ILPQYNNISVE		TADSETVH--		--YHYGPKDL		VTILEYIFIT		IIIIHAVVQEY	100
HWAR1.AMI	51	LTLQHSVAVP		AAEEQATGSK		SLYYGVGKDL		ATVFEFVMLVA		IIIIHATIQEY	100
RWAR1.AMI	51	LTLQHGWWVE		A-EGLPSGSR		TLYHYGVKDL		ATVFEFVMLVA		IIIIHATIQEY	100
			110		120		130		140		150
HTRAM.AMI	101	MLDKINRRMH		FSKTKHSKEN		ESGOLSAEYL		FAQVNGTFIL		ISENYISDPT	150
KIAA0057.AMI	101	ILDKISKRLH		LSKVVKHSKEN		ESGOLVVEHE		TSVINGCFVW		VTGYLTNER	150
HWAR1.AMI	101	VLDKINKRMQ		FTKAKQNKEN		ESGQFSVFEY		FSCINGTFIL		ISENCLSDPT	150
RWAR1.AMI	101	VLDKLSRRLQ		LTKGKQNKLN		EAGOLSVEYI		VSCINGMTIL		ASENCLSDPT	150
			160		170		180		190		200
HTRAM.AMI	151	ILWRAYPHNL		MTEQMKFFYI		SOLAYMLHAF		PELYEQTKK		EDIPROLVYI	200
KIAA0057.AMI	151	SLMEDYPHVH		LPEQVKFFYL		CQLAYMLHAL		PELYEQVRK		EETPRQLQYT	200
HWAR1.AMI	151	LIWKARPHSM		MTEQMKFFYI		SOLAYMFHAF		PELYEQTKK		QDIPROLVYI	200
RWAR1.AMI	151	LLWKSQPHNM		MTEQMKFFYI		SOLAYMFHSE		PELYEQVRK		QDIPCOLIYI	200
			210		220		230		240		250



Fig. 2 (cont.)

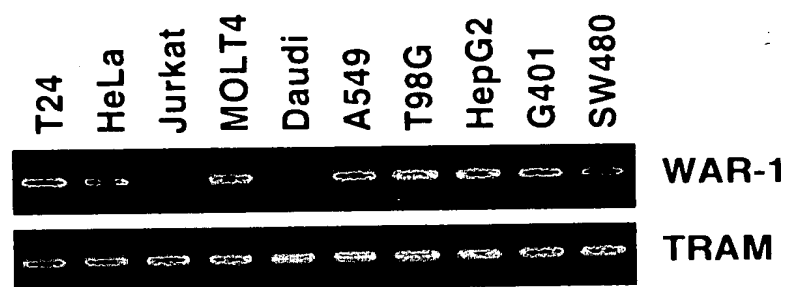
HTRAM.AMI	201	GLYLEHIAGA	YLLNHNHGL	VLLVLYHYVE	FLFHISRLFY	ESNEKYOKGE	250
KIAA0057.AMI	201	CLYLVHIAGA	YLLNHSRGL	ILLIQJSTE	FLFHTARLFY	FADENNEKLE	250
HWAR1.AMI	201	GLHLEHIITGA	YLLYLNHGL	LLLVLYHYVE	LSSHMCGLFY	ESDEKYOKGI	250
RWAR1.AMI	201	GLHLEHIICGA	YLLYLNHGL	LLLMHYHVE	LSSVCSLLY	EGDERYOKGL	250
			260	270	280	290	300
HTRAM.AMI	251	SLMAVLEVLG	RLTLILSVL	TVGEGLARME	NOKLDFSTGN	FNVLAIRIAY	300
KIAA0057.AMI	251	SAMAAVFGVT	RLFILTLAVI	AIGEGLARME	NOAFDPEKGN	FNTLFCRLQV	300
HWAR1.AMI	251	SLWAIIVFILG	RLVTLIVSVL	TVGEGHLAGSQ	NRNPDALTGN	VNVLAAKIAY	300
RWAR1.AMI	251	SIMPPIVFISG	RLVTLIVSVV	TVGLHLTAGT	NRNGNALSGN	VNVLAAKIAY	300
			310	320	330	340	350
HTRAM.AMI	301	LASICVTQAF	MMWKFINFQL	RWRREHSAFO	APAVKKKFTV	TK--GRSSKK	350
KIAA0057.AMI	301	LLLVCAAQAM	LMWRFJHSQL	RHWREYWN-E	QSAKRRRVFAT	PRLPARLIKR	350
HWAR1.AMI	301	LSSSCTIQAY	VTWNLITLWL	QRWVEDSNIQ	ASCMKKK---	-R--SRSSKK	350
RWAR1.AMI	301	LSSSCSIQVY	ITWTLTIVWL	QRWLEDANLH	V-CGRKR---	-R--SRS---	350
			360	370	380	390	400
HTRAM.AMI	351	GTENGUNGTL	TSNVADSPRN	KKEKSS....	400
KIAA0057.AMI	351	ESGYHENGW	KAENGTSPT	KKLKSP....	400
HWAR1.AMI	351	RTENGV-GVE	TSNRVDCPPK	RKEKSS....	400
RWAR1.AMI	351	RKGTEN-GVE	NPNRIDSPPK	KKEKAP....	400



09/807470

7/15

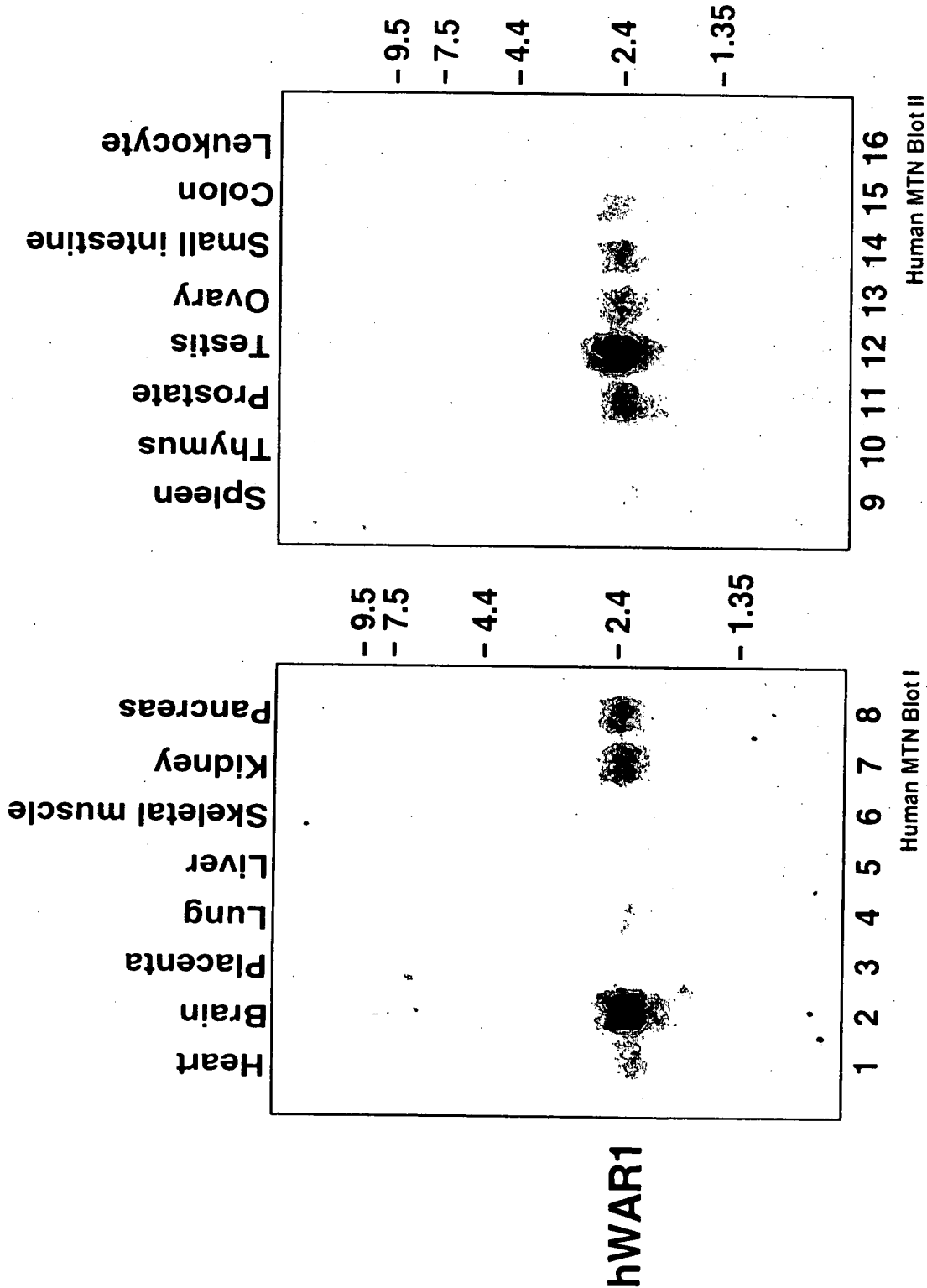
Fig. 3

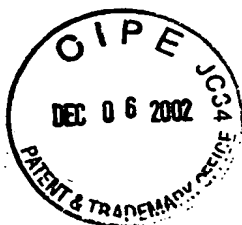




8/15

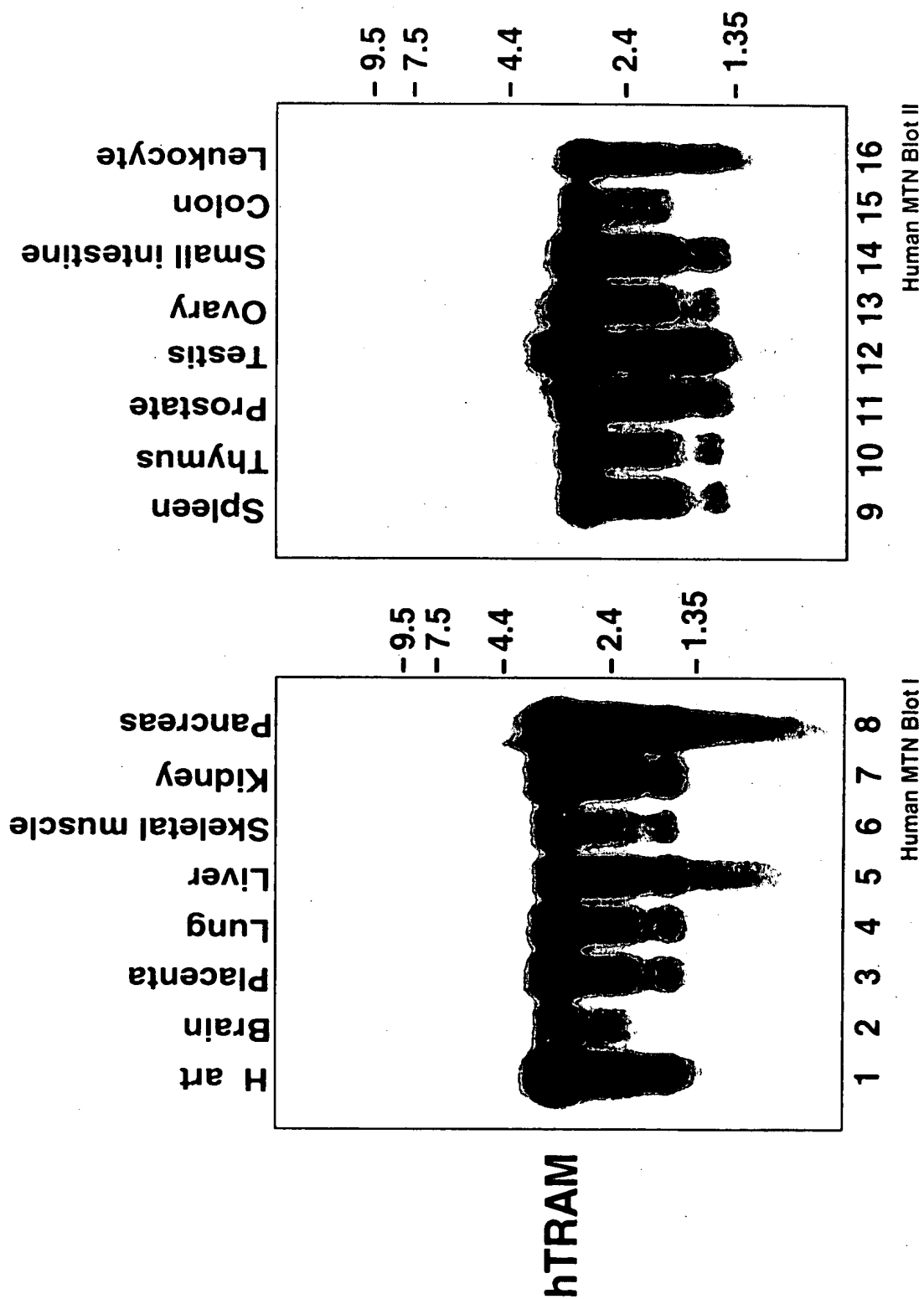
Fig. 4





9/15

Fig. 5

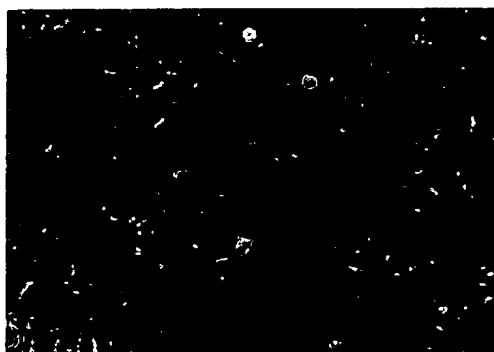




10/15

Fig. 6

A



B



C



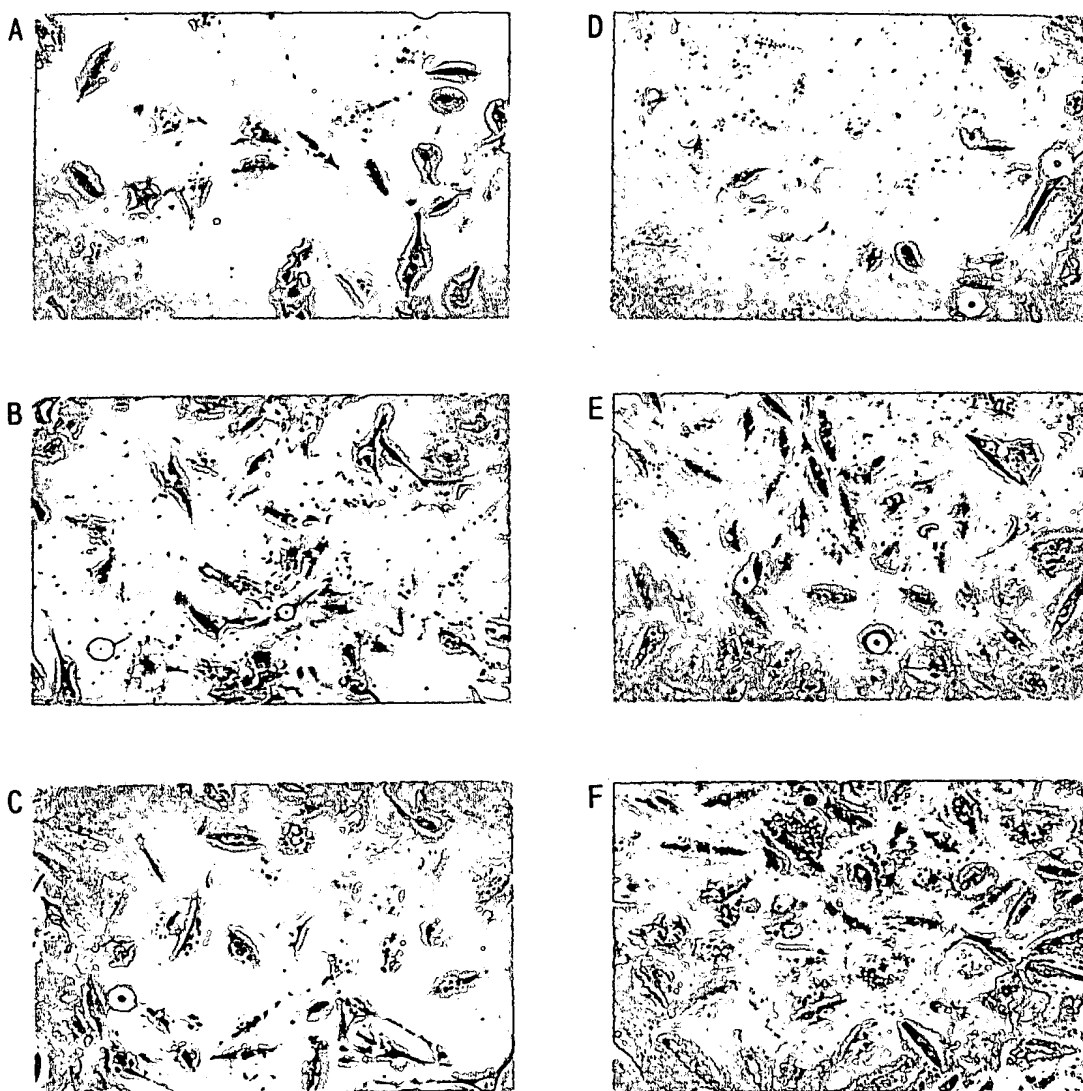
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11/15

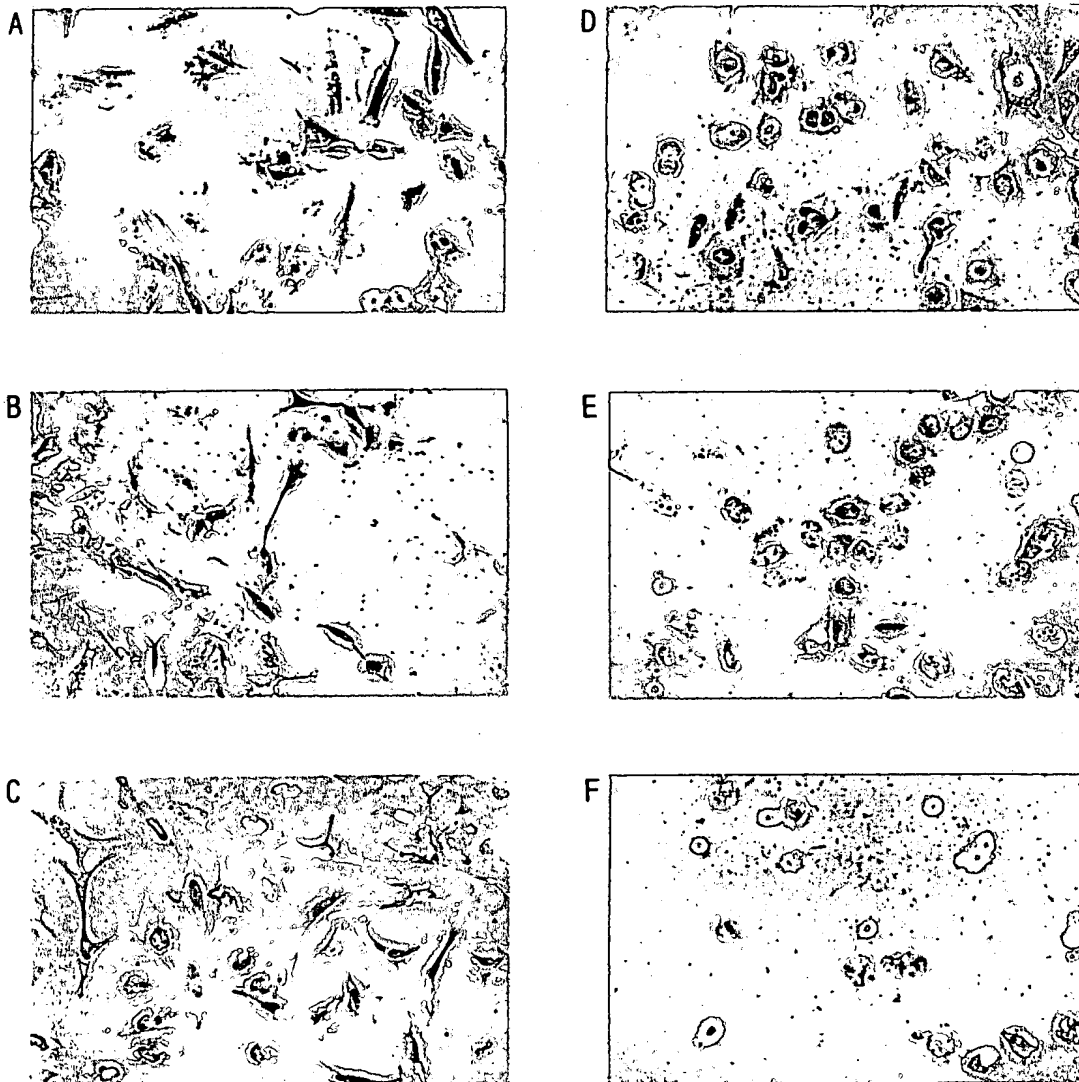
Fig. 7





12/15

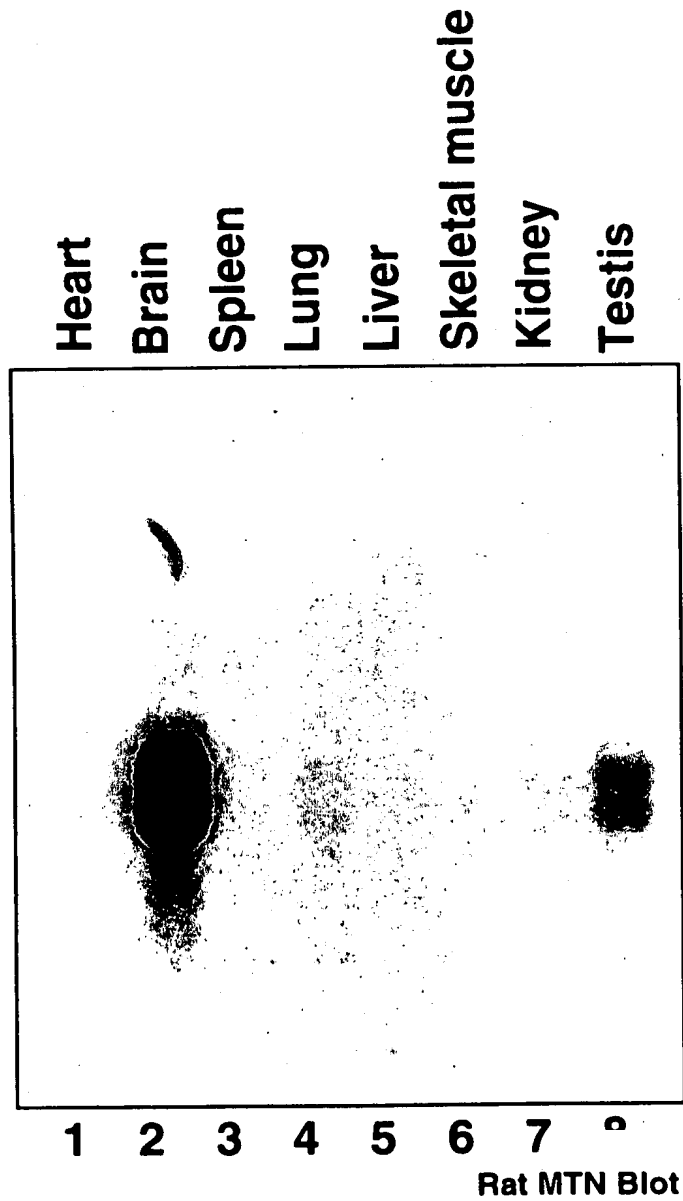
Fig. 8





13/15

Fig. 9

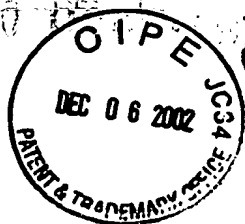




14/15

Fig. 1 0





09/807470

15/15

Fig. 1 1

